



Estimation of variance components, genetic parameters and genetic trends for litter size of swines

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ABSTRACT - Records of Large White breed animals were used to estimate variance components, genetic parameters and trends for the character total number of born piglets (TNBP) as measure of litter size. For obtaining variance components and genetic parameters, it was used the Restricted Maximum Likelihood Method using MTDFREML software. Two mixed models (additive and repeatability) were evaluated. The additive model contained fixed effect of the contemporary group and the following random effects: direct additive genetic and residual effect for the first parturition. Repeatability model had the same effects of the additive model plus parturition order fixed effect and non-correlated animal permanent environment random effect for the second, third and fourth parturition. Direct additive heritability estimates for TNBP were 0.15 and 0.20 for the additive and repeatability models, respectively. The estimate of the ratio among variance of the non-correlated effect of animal permanent environment effect and the phenotypic variance, expressed as total variance proportion (c^2) was 0.09. The estimates of yearly genetic trends obtained in the additive and repeatability models have similar behaviors (0.02 piglets/sow/year).

Key Words: genetic trend, heritability, number of piglets, REML, repeatability model, reproductive traits

Estimação de parâmetros genéticos, componentes de variância e tendências genéticas em tamanho de leitegada de suínos

RESUMO - Registros de animais da raça Large White foram usados para estimar componentes de variância, parâmetros e tendências genéticas para a característica número total de leitões nascidos (NLT) como medida do tamanho de leitegada. Na obtenção dos componentes de variância e parâmetros genéticos, foi utilizado o método da Máxima Verossimilhança Restrita, por meio do programa MTDFREML. Foram avaliados dois modelos mistos (aditivo e de repetibilidade). O modelo aditivo continha efeito fixo de grupo contemporâneo e os seguintes efeitos aleatórios: genético aditivo direto e residual para o primeiro parto. O modelo de repetibilidade continha os mesmos efeitos do modelo aditivo mais o efeito fixo de ordem de parto e o efeito aleatório não-correlacionado de ambiente permanente do animal para o segundo, terceiro e quarto parto. As estimativas de herdabilidades aditivas diretas para NLT foram de 0,15 e 0,20 para os modelos aditivo e de repetibilidade, respectivamente. A estimativa da razão entre a variância do efeito não-correlacionado de ambiente permanente do animal e a variância fenotípica, expressa como proporção da variância total (c^2), foi de 0,09. As estimativas de tendências genéticas anuais obtidas nos modelos aditivos e de repetibilidade têm comportamentos similares (em torno de 0,02 leitão/fêmea/ano).

Palavras-chave: características reprodutivas, herdabilidade, modelo de repetibilidade, número de leitões nascidos, REML, tendência genética

Introduction

Over the last few years, swine improvement programs have emphasized the selection of fertility traits in female lines (Sorensen et al., 2000). Although it has been recognized that fertility comprises a set of traits, an effort to improve the reproductive performance of sows has been directed at the selection for litter size. Some studies have indicated litter size

as the most important economic component of reproductive performance in sows (Smith et al., 1983; Tess et al., 1983).

Heritability estimates for litter size reported in the literature range from 0.00 to 0.76 (Rothschild & Bidanel, 1998). These variations are due to the number and quality of the records and the models and estimation methods used. Additionally, there are some controversies in the literature as to whether litter size in different parities should

be considered as repeated measurements of the same trait (Southwood & Kennedy, 1990; See et al., 1993; Crump et al., 1997; Lourenço et al., 2008) or as different traits (Irgang et al., 1994; Roehe & Kennedy, 1995; Rydhmer et al., 1995; Barbosa et al., 2008).

The magnitude of the genetic correlation between parities is important for a better genetic evaluation process in selection programs. In the literature, the genetic correlation for litter size among parities generally exceeds 0.70 between the first and subsequent parities (Knap et al., 1993; Irgang et al., 1994; Roehe & Kennedy, 1995; Tholen et al., 1996; Alfonso et al., 1997; Hanenberg et al., 2001).

According to Lukoviæ et al. (2004), litter size at first parity should be considered to be genetically different from litter size in subsequent parities because of the variation in the genetic correlation between the first and subsequent parities which ranges from 0.66 to 0.80. Low genetic correlations between the first and second or third parity (0.55 to 0.74) were also reported by Alfonso et al. (1994) and Hermesch et al. (2000). According to Duc et al. (1998), these moderate genetic correlations between the first and subsequent parities indicate a slight difference in genetic control at first parity. However, Hermesch et al. (2000) observed a high genetic correlation (0.95) for litter size between the second and third parity and suggested that these traits (second and subsequent parities) should be treated as repeated measures.

The objective of the present study was to estimate variance components, genetic parameters, and genetic trends for litter size in a swine population.

Material and Methods

Data from Large White pigs belonging to a farm located in the western region of Santa Catarina state were used in this study (Table 1). The animals were born from 1996 to 2006.

The trait total number of born piglets was evaluated as a measure of litter size. Only records of the first four parities were used due to the small number of records for the subsequent parities since the studied farm was a nucleus herd.

Contemporary group formed by the combination of year and week of farrowing of the animal and parity order were used as fixed effects.

The variance components were estimated by the restricted maximum likelihood method using the MTDREML program (Boldman et al., 1995). The following models were used:

- Additive model (1st parity):

$$y_{ij} = \mu + GC_i + d_j + e_{ij}$$

where: y_{ij} = trait observed in animal j of contemporary group i ; μ = general mean; GC_i = fixed effect of contemporary group i ; d_j = additive random effect of animal j ; e_{ij} = random error.

- Repeatability model (2nd, 3rd and 4th parities):

$$y_{ijkl} = \mu + GC_i + OP_j + d_k + p_l + e_{ijkl}$$

where OP_j = fixed effect of parity order j ; p_l = random permanent environmental effect of animal l . The remaining terms are defined in the additive model.

The matrix representation of the models is:

$$\text{model 1: } y = Xb + Z_1 d + e,$$

$$\text{model 2: } y = Xb + Z_1 d + Z_2 p + e,$$

in which y = vector of observations; b = vector of fixed effects; X = incidence matrix of fixed effects; d = vector of random additive genetic effects; Z_1 = incidence matrix of random genetic effects; p = vector of random permanent environmental effects; Z_2 = incidence matrix of random permanent environmental effect; e = vector of random residual effects.

The assumptions for random effects are:

$$\begin{bmatrix} d \\ p \\ e \end{bmatrix} \sim NMV \left\{ \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}; \begin{bmatrix} G & \phi & \phi \\ \phi & P & \phi \\ \phi & \phi & R \end{bmatrix} \right\}$$

in which $G = A\sigma_a^2$, with A being the numerator relationship matrix among animals and σ_a^2 the additive genetic variance; $P = I\sigma_c^2$, with I being an identity matrix and σ_c^2 the permanent environmental variance; $R = I\sigma_e^2$, with σ_e^2 being the residual variance; and ϕ a matrix of zeros (Searle, 1971).

Table 1 - Data structure and mean and standard deviation of number of piglets born to Large White sows obtained using the additive and repeatability models

Item	Value	
	Additive model	Repeatability model
Number of animals in A ⁻¹	58,628	58,628
Total number of records	3,196	3,355
2 nd parity	—	1,707
3 rd parity	—	1,061
4 th parity	—	587
Number of contemporary groups	517	506
Number of sows	1,604	1,067
Number of boars	370	322
Total number of piglets born		
Mean	10.98	11.15
Standard deviation	3.23	3.47
Coefficient of variation (%)	29.41	31.09

Each analysis was restarted with different initial values to guarantee that the values of the estimated components corresponded to the absolute maximum of the likelihood function, in an attempt to prevent convergence to local maxima. Simplex variance lower than 10^{-9} was defined as a convergence criterion.

The genetic trend in litter size was calculated by linear regression of mean breeding values of animals born between 1993 and 2006 (all animals of the relationship matrix) for number of piglets born as a function of year of birth of the animals (Table 1).

Results and Discussion

The estimates of heritability and additive genetic and phenotypic variances obtained with the repeatability model were greater than those estimated with the additive model (Table 2). However, residual variance was greater when estimated by the additive model (Table 2). These results suggest that the genetic control at first parity is different or different genes could be affecting the litter size at first and subsequent parities. Thus, according to the estimates of heritability and additive genetic and the obtained phenotypic variances, the use of an additive model for first parity and a repeatability model for subsequent parities should be recommended in the genetic evaluation of this trait.

The estimate of permanent environmental variance was greater than those reported by Ehlers et al. (2005), who observed values ranging from 0.00 to 0.011 for number of piglets born alive in crossbred and purebred pigs.

Considering that heritability estimates for litter size in pigs have shown variations in magnitude depending on the breed, model and volume of data analyzed, genetic

evaluation of the populations for this trait should take into account all these aspects in order to optimize the genetic gain. Haley et al. (1988) concluded that the heritability of litter size is generally approximately 0.09. In Landrace pigs, Hanenberg et al. (2001) found heritability estimates for number of piglets born at first parity of 0.093 (additive model) and 0.101 (repeatability model), values lower than those obtained in the present study. Ehlers et al. (2005), using a repeatability model that included first parity records of Large White pigs, also reported heritability estimates lower than those obtained with the present repeatability model (0.155). Results similar to those of the present study have been reported by Kaufmann et al. (2000) who obtained heritability estimates of 0.22 in Large White animals.

See et al. (1993), studying three purebred breeds and using a model that only included first parity records, observed heritability estimates for number of pigs born alive of about 0.13. Ferraz & Johnson (1993) reported heritabilities of 0.14 for number of piglets born alive in Large White pigs using a model that only included additive effects and Barbosa et al. (2008), using data from the first four parities of Large White sows, estimated heritabilities in single and multiple trait analyses ranged from 0.14 to 0.20. These results are similar to those found in the present study. However, Roehe & Kennedy (1995) and Holm et al. (2005) reported heritability estimates for number of piglets born of about 0.10 when using a model that only included first parity records of Landrace pigs.

The estimated ratio of permanent environmental variance (c^2) found in the present study is within the interval of estimates (0.00 to 0.19) reported in the literature for number of born piglets (Lamberson et al., 1991; Knap et al., 1993; Estany & Sorensen, 1994; Lourenço et al., 2008).

According to Euclides Filho et al. (1997), it is essential to monitor cumulative genetic progresses in selection programs not only to quantify the occurrence of genetic changes but mainly to evaluate benefits and to perform adjustments when necessary. Thus, it is necessary to know the genetic trend of the population studied.

The estimates of annual genetic trends in litter size at birth were positive, in agreement with the objective of a genetic improvement program for this trait. However, the genetic progress over the years was very small (0.02 piglets/sow/year), suggesting that selection for this trait was not effective or that little attention was paid to this trait during the analyzed period. Pires et al. (2000) and Lourenço et al. (2008) reported poorly expressive genetic trends for this trait in Large White pigs (respectively, 0.0279 and 0.0019 piglets/sow/year), whereas Southwood & Kennedy (1991) observed even lower and negative annual

Table 2 - Variance component and genetic parameter estimates for total number of piglets born obtained in the evaluation of Large White sows

Parameter	Additive model	Repeatability model
σ_d^2	1.57	2.35
σ_c^2	—	1.12
σ_e^2	8.73	8.41
σ_p^2	10.31	11.88
h^2	0.15 (0.034)*	0.20 (0.038)*
c^2	—	0.094 (0.037)*

σ_d^2 = additive genetic variance; σ_c^2 = variance of animal permanent environmental effects; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h^2 = heritability; c^2 = ratio of permanent environmental variance.
* Standard error.

genetic trends (-0.004) for litter size at birth in Large White swine. On the other hand, Bidanel et al. (1994) and Johnson (1992) reported highly relevant trends of 0.7 and 1.8 piglets per litter, respectively.

Irgang et al. (1997), studying the number of piglets born alive in the first two litters of Landrace and Large White pigs, observed positive, but small, genetic trends. The authors concluded that low selection intensity was applied to the genetic improvement of this trait in these breeds in Brazil. Thus, the present results agree with those obtained by Irgang et al. in the 1990s.

The low genetic progress of reproductive traits can mainly be explained by two factors. First, reproductive traits generally remain as low priority when considering selection criteria. The second factor is the low heritability of these traits which impairs genetic progress. However, despite the difficulties encountered when using reproductive traits, at least litter size at birth should be more emphasized as one of the selection criteria in Large White pigs which are commonly used as the maternal line in crossing schemes.

Conclusions

The use of an additive model for first parity and of a repeatability model for subsequent parities is recommended in the genetic evaluation of pigs for litter size. Furthermore, litter size at birth should be included as a selection trait in Large White pigs.

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